

SEQUENCE LISTING

(1) GENERAL INFORMATION

- 5 (i) APPLICANT: University of Utrecht, Technology Foundation
- (ii) TITLE OF THE INVENTION: Vaccine
- (iii) NUMBER OF SEQUENCES: 10
- 10 (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: SmithKline Beecham, Corporate IP Department
- (B) STREET: Two, New Horizons Court,
- (C) CITY: Brentford
- 15 (D) STATE: Middlesex
- (E) COUNTRY: United Kingdom
- (F) ZIP: TW8 9EP
- (v) COMPUTER READABLE FORM:
- 20 (A) MEDIUM TYPE: Diskette
- (B) COMPUTER: IBM Compatible
- (C) OPERATING SYSTEM: DOS
- (D) SOFTWARE: FastSEQ for Windows Version 2.0
- 25 (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER:
- (B) FILING DATE:
- (C) CLASSIFICATION:
- 30 (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER:
- (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
- 35 (A) NAME: DALTON, Marcus Jonathan William
- (B) REGISTRATION NUMBER: XXXXXX
- (C) REFERENCE/DOCKET NUMBER: B45106
- (ix) TELECOMMUNICATION INFORMATION:
- 40 (A) TELEPHONE: (0181) 975 6348
- (B) TELEFAX: (0181) 975 6177

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 2277 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(B) STRAIN: *Neisseria meningitidis* strain BNCV

(ix) FEATURE:

15 (A) NAME/KEY: Coding Sequence

(B) LOCATION: 100...2274

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

20 TCCTGATTTT TGTTAATTCA CTATAAAAAC GGGTTGATAT TATCTGTACA TATTAATATA 60
 ATGATAATTA TTATTAATCA AATAGGAGGA AAAGTAGGG ATG TGT AAA CCG AAT 114
 Met Cys Lys Pro Asn
 1 5

25 TAT GGC GGC ATT GTC TTG TTG CCC TTA CTT TTG GCA TCT TGT ATC GGC 162
 Tyr Gly Gly Ile Val Leu Leu Pro Leu Leu Ala Ser Cys Ile Gly
 10 15 20

30 GGC AAT TTC GGC GTG CAG CCT GTT GTC GAA TCA ACG CCG ACC GCG TAC 210
 Gly Asn Phe Gly Val Gln Pro Val Val Glu Ser Thr Pro Thr Ala Tyr
 25 30 35

35 CCC GTC ACT TTC AAG TCT AAG GAC GTT CCC ACT CCG CCC CCT GCC AAA 258
 Pro Val Thr Phe Lys Ser Lys Asp Val Pro Thr Pro Pro Pro Ala Lys
 40 45 50

40 CCT TCT ATA GAA ATC ACG CCG GTC AAC CGG CCC GCC GTC GGT GCG GCA 306
 Pro Ser Ile Glu Ile Thr Pro Val Asn Arg Pro Ala Val Gly Ala Ala
 55 60 65

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|----|---|-----|
| | ATG CGG CTG CCA AGG CGG AAT ACT GCT TTT CAT CGT GAA GAT GGC ACG | 354 |
| | Met Arg Leu Pro Arg Arg Asn Thr Ala Phe His Arg Glu Asp Gly Thr | |
| | 70 75 80 85 | |
| 5 | GAA ATT CCA AAT AGC AAA CAA GCA GAA GAA AAG CTG TCG TTT CAA GAA | 402 |
| | Glu Ile Pro Asn Ser Lys Gln Ala Glu Glu Lys Leu Ser Phe Gln Glu | |
| | 90 95 100 | |
| 10 | GGT GAT GTT CTG TTT TTA TAC GGT TCA AAA GGA AAT AAA CTT CAA CAA | 450 |
| | Gly Asp Val Leu Phe Leu Tyr Gly Ser Lys Gly Asn Lys Leu Gln Gln | |
| | 105 110 115 | |
| 15 | CTT AAA AGC GAA ATT CAT AAA CGT GAT TCC GAT GTA GAA ATT AGG ACA | 498 |
| | Leu Lys Ser Glu Ile His Lys Arg Asp Ser Asp Val Glu Ile Arg Thr | |
| | 120 125 130 | |
| 20 | TCA GAA AAG GAA AAT AAA AAA TAT GAT TAT AAA TTT GTA GAT GCA GGT | 546 |
| | Ser Glu Lys Glu Asn Lys Lys Tyr Asp Tyr Lys Phe Val Asp Ala Gly | |
| | 135 140 145 | |
| 25 | TAT GTA TAT GTA AAG GGA AAA GAT GAA ATT AAG TGG ACT TCA GAT TAC | 594 |
| | Tyr Val Tyr Val Lys Gly Lys Asp Glu Ile Lys Trp Thr Ser Asp Tyr | |
| | 150 155 160 165 | |
| 30 | AAG CAG TTT TCC AAC CGC TTA GGT TAT GAC GGT TTT GTA TAT TAT TCC | 642 |
| | Lys Gln Phe Ser Asn Arg Leu Gly Tyr Asp Gly Phe Val Tyr Tyr Ser | |
| | 170 175 180 | |
| 35 | GGA GAA CGT CCT TCC CAA TCT TTA CCG AGT GCG GGA ACG GTG GAA TAT | 690 |
| | Gly Glu Arg Pro Ser Gln Ser Leu Pro Ser Ala Gly Thr Val Glu Tyr | |
| | 185 190 195 | |
| 40 | TCT GGT AAC TGG CAA TAT ATG ACC GAT GCC AAA CGT CAT CGA GCA GGT | 738 |
| | Ser Gly Asn Trp Gln Tyr Met Thr Asp Ala Lys Arg His Arg Ala Gly | |
| | 200 205 210 | |
| 45 | AAG GCG GTT GGC ATT GAC AAT TTG GGT TAT TAC ACA TTT TAT GGT AAC | 786 |
| | Lys Ala Val Gly Ile Asp Asn Leu Gly Tyr Tyr Thr Phe Tyr Gly Asn | |
| | 215 220 225 | |
| 50 | GAT GTT GGT GCA ACT TCT TAT GCG GCT AAG GAT GTC GAC GAA AGG GAA | 834 |
| | Asp Val Gly Ala Thr Ser Tyr Ala Ala Lys Asp Val Asp Glu Arg Glu | |
| | 230 235 240 245 | |

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|----|---|------|
| | AAA CAT CCT GCT AAA TAT ACG GTA GAT TTC GGT AAC AAA ACC CTG ACG | 882 |
| | Lys His Pro Ala Lys Tyr Thr Val Asp Phe Gly Asn Lys Thr Leu Thr | |
| | 250 255 260 | |
| 5 | GGC GAG CTG ATT AAA AAC CAA TAT GTC AAA CCC AGT GAG AAG CAA AAA | 930 |
| | Gly Glu Leu Ile Lys Asn Gln Tyr Val Lys Pro Ser Glu Lys Gln Lys | |
| | 265 270 275 | |
| 10 | CCG CTG ACC ATT TAC AAC ATC ACT GCC GAT TTA AAC GGC AAC CGC TTT | 978 |
| | Pro Leu Thr Ile Tyr Asn Ile Thr Ala Asp Leu Asn Gly Asn Arg Phe | |
| | 280 285 290 | |
| 15 | ACC GGC AGT GCC AAG GTC AAT CCT GAT TTA GCG AAA AGC CAT GCC AAT | 1026 |
| | Thr Gly Ser Ala Lys Val Asn Pro Asp Leu Ala Lys Ser His Ala Asn | |
| | 295 300 305 | |
| 20 | AAG GAG CAT TTG TTT TTC CAT GCC GAT GCC GAT CAG CGG CTT GAG GGC | 1074 |
| | Lys Glu His Leu Phe Phe His Ala Asp Ala Asp Gln Arg Leu Glu Gly | |
| | 310 315 320 325 | |
| 25 | GGT TTT TTC GGC GAT AAG GGG GAA GAG CTT GCC GGA CGG TTT ATC AGC | 1122 |
| | Gly Phe Phe Gly Asp Lys Gly Glu Glu Leu Ala Gly Arg Phe Ile Ser | |
| | 330 335 340 | |
| 30 | AAC GAC AAC AGC GTA TTC GGT GTA TTC GCA GGC AAA CAA AAT AGC CCC | 1170 |
| | Asn Asp Asn Ser Val Phe Gly Val Phe Ala Gly Lys Gln Asn Ser Pro | |
| | 345 350 355 | |
| 35 | GTT GAT GAG GCA AGT GGT GAA AAT CCC CGA CCG TTT GCC ATT TCT CCT | 1266 |
| | Val Asp Glu Ala Ser Gly Glu Asn Pro Arg Pro Phe Ala Ile Ser Pro | |
| | 375 380 385 | |
| 40 | ATG CCC GAT TTT GGT CAT CCC GAC AAA CTT CTT GTC GAA GGG CAT GAA | 1314 |
| | Met Pro Asp Phe Gly His Pro Asp Lys Leu Leu Val Glu Gly His Glu | |
| | 390 395 400 405 | |

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|----|---|------|
| | ATT CCT TTG GTT AGC CAA GAG AAA ACC ATC GAG CTT GCC GAC GGC AGG | 1362 |
| | Ile Pro Leu Val Ser Gln Glu Lys Thr Ile Glu Leu Ala Asp Gly Arg | |
| | 410 415 420 | |
| 5 | AAA ATG ACC GTC AGT GCT TGT TGC GAC TTT TTG ACC TAT GTG AAA CTC | 1410 |
| | Lys Met Thr Val Ser Ala Cys Cys Asp Phe Leu Thr Tyr Val Lys Leu | |
| | 425 430 435 | |
| 10 | GGA CGG ATA AAA ACC GAA CGC CCC GCC GCC AAA CCG AAG GCG CAG GAC | 1458 |
| | Gly Arg Ile Lys Thr Glu Arg Pro Ala Ala Lys Pro Lys Ala Gln Asp | |
| | 440 445 450 | |
| 15 | GAA GAG GAT TCG GAC ATT GAT AAT GGC GAA GAA AGC GAA GAC GAA ATC | 1506 |
| | Glu Glu Asp Ser Asp Ile Asp Asn Gly Glu Glu Ser Glu Asp Glu Ile | |
| | 455 460 465 | |
| 20 | GGC GAT GAA GAA GAA GGC ACC GAA GAT GCA GCC GCA GGA GAT GAA GGC | 1554 |
| | Gly Asp Glu Glu Glu Gly Thr Glu Asp Ala Ala Ala Gly Asp Glu Gly | |
| | 470 475 480 485 | |
| 25 | AGC GAA GAA GAC GAA GCC ACA GAA AAC GAA GAC GGC GAA GAA GAC GAA | 1602 |
| | Ser Glu Glu Asp Glu Ala Thr Glu Asn Glu Asp Gly Glu Glu Asp Glu | |
| | 490 495 500 | |
| 30 | GCT GAA GAA CCT GAA GAA GAA TCG TCG GCA GAA GGC AAC GGC AGT TCA | 1650 |
| | Ala Glu Glu Pro Glu Glu Glu Ser Ser Ala Glu Gly Asn Gly Ser Ser | |
| | 505 510 515 | |
| 35 | AAC GCC ATC CTG CCT GTC CCG GAA GCC TCT AAA GGC AGG GAT ATC GAC | 1698 |
| | Asn Ala Ile Leu Pro Val Pro Glu Ala Ser Lys Gly Arg Asp Ile Asp | |
| | 520 525 530 | |
| 40 | CTT TTC CTG AAA GGT ATC CGC ACG GCA GAA ACG AAT ATT CCG CAA ACT | 1746 |
| | Leu Phe Leu Lys Gly Ile Arg Thr Ala Glu Thr Asn Ile Pro Gln Thr | |
| | 535 540 545 | |
| 45 | GGA GAA GCA CGC TAT ACC GGC ACT TGG GAA GCG CGT ATC GGC AAA CCC | 1794 |
| | Gly Glu Ala Arg Tyr Thr Gly Thr Trp Glu Ala Arg Ile Gly Lys Pro | |
| | 550 555 560 565 | |
| 50 | ATT CAA TGG GAC AAT CAT GCG GAT AAA GAA GCG GCA AAA GCA GTA TTT | 1842 |
| | Ile Gln Trp Asp Asn His Ala Asp Lys Glu Ala Ala Lys Ala Val Phe | |
| | 570 575 580 | |

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|----|---|------|
| | ACC GTT GAT TTC GGC AAG AAA TCG ATT TCC GGA ACG CTG ACG GAG AAA | 1890 |
| | Thr Val Asp Phe Gly Lys Lys Ser Ile Ser Gly Thr Leu Thr Glu Lys | |
| | 585 590 595 | |
| 5 | AAC GGT GTA GAA CCT GCT TTC CGT ATT GAA AAC GGC GTG ATT GAG GGC | 1938 |
| | Asn Gly Val Glu Pro Ala Phe Arg Ile Glu Asn Gly Val Ile Glu Gly | |
| | 600 605 610 | |
| 10 | AAC GGT TTC CAT GCG ACA GCG CGC ACT CGG GAT GAC GGC ATC GAC CTT | 1986 |
| | Asn Gly Phe His Ala Thr Ala Arg Thr Arg Asp Asp Gly Ile Asp Leu | |
| | 615 620 625 | |
| 15 | TCC GGG CAG GGT TCG ACC AAA CCG CAG ATC TTC AAA GCT AAT GAT CTT | 2034 |
| | Ser Gly Gln Gly Ser Thr Lys Pro Gln Ile Phe Lys Ala Asn Asp Leu | |
| | 630 635 640 645 | |
| 20 | CGT GTA GAA GGA GGA TTT TAC GGC CCG AAG GCG GAG GAA TTG GGC GGT | 2082 |
| | Arg Val Glu Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu Gly Gly | |
| | 650 655 660 | |
| 25 | ATT ATT TTC AAT AAT GAT GGG AAA TCT CTT GGT ATA ACT GAA GGT ACT | 2130 |
| | Ile Ile Phe Asn Asn Asp Gly Lys Ser Leu Gly Ile Thr Glu Gly Thr | |
| | 665 670 675 | |
| 30 | GAA AAT AAA GTT GAA GCT GAT GTT GAT GTT GAT GTT GAT GTT GAT GTT | 2178 |
| | Glu Asn Lys Val Glu Ala Asp Val Asp Val Asp Val Asp Val Asp Val | |
| | 680 685 690 | |
| 35 | GAT GCT GAT GCT GAT GTT GAA CAG TTA AAA CCT GAA GTT AAA CCC CAA | 2226 |
| | Asp Ala Asp Ala Asp Val Glu Gln Leu Lys Pro Glu Val Lys Pro Gln | |
| | 695 700 705 | |
| 35 | TTC GGC GTG GTA TTC GGT GCG AAG AAA GAT AAT AAA GAG GTG GAA AAA T | 2275 |
| | Phe Gly Val Val Phe Gly Ala Lys Lys Asp Asn Lys Glu Val Glu Lys | |
| | 710 715 720 725 | |
| | GA | 2277 |

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 725 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(B) STRAIN: Neisseria meningitidis strain BNCV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Cys Lys Pro Asn Tyr Gly Gly Ile Val Leu Leu Pro Leu Leu Leu
 1             5             10             15
Ala Ser Cys Ile Gly Gly Asn Phe Gly Val Gln Pro Val Val Glu Ser
      20             25             30
20 Thr Pro Thr Ala Tyr Pro Val Thr Phe Lys Ser Lys Asp Val Pro Thr
      35             40             45
Pro Pro Pro Ala Lys Pro Ser Ile Glu Ile Thr Pro Val Asn Arg Pro
      50             55             60
Ala Val Gly Ala Ala Met Arg Leu Pro Arg Arg Asn Thr Ala Phe His
25 65             70             75             80
Arg Glu Asp Gly Thr Glu Ile Pro Asn Ser Lys Gln Ala Glu Glu Lys
      85             90             95
Leu Ser Phe Gln Glu Gly Asp Val Leu Phe Leu Tyr Gly Ser Lys Gly
      100            105            110
30 Asn Lys Leu Gln Gln Leu Lys Ser Glu Ile His Lys Arg Asp Ser Asp
      115            120            125
Val Glu Ile Arg Thr Ser Glu Lys Glu Asn Lys Lys Tyr Asp Tyr Lys
      130            135            140
Phe Val Asp Ala Gly Tyr Val Tyr Val Lys Gly Lys Asp Glu Ile Lys
35 145            150            155            160
Trp Thr Ser Asp Tyr Lys Gln Phe Ser Asn Arg Leu Gly Tyr Asp Gly
      165            170            175

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Phe Val Tyr Tyr Ser Gly Glu Arg Pro Ser Gln Ser Leu Pro Ser Ala
 180 185 190
 Gly Thr Val Glu Tyr Ser Gly Asn Trp Gln Tyr Met Thr Asp Ala Lys
 195 200 205
 5 Arg His Arg Ala Gly Lys Ala Val Gly Ile Asp Asn Leu Gly Tyr Tyr
 210 215 220
 Thr Phe Tyr Gly Asn Asp Val Gly Ala Thr Ser Tyr Ala Ala Lys Asp
 225 230 235 240
 Val Asp Glu Arg Glu Lys His Pro Ala Lys Tyr Thr Val Asp Phe Gly
 10 245 250 255
 Asn Lys Thr Leu Thr Gly Glu Leu Ile Lys Asn Gln Tyr Val Lys Pro
 260 265 270
 Ser Glu Lys Gln Lys Pro Leu Thr Ile Tyr Asn Ile Thr Ala Asp Leu
 275 280 285
 15 Asn Gly Asn Arg Phe Thr Gly Ser Ala Lys Val Asn Pro Asp Leu Ala
 290 295 300
 Lys Ser His Ala Asn Lys Glu His Leu Phe Phe His Ala Asp Ala Asp
 305 310 315 320
 Gln Arg Leu Glu Gly Gly Phe Phe Gly Asp Lys Gly Glu Glu Leu Ala
 20 325 330 335
 Gly Arg Phe Ile Ser Asn Asp Asn Ser Val Phe Gly Val Phe Ala Gly
 340 345 350
 Lys Gln Asn Ser Pro Val Pro Ser Gly Lys His Thr Lys Ile Leu Asp
 355 360 365
 25 Ser Leu Lys Ile Ser Val Asp Glu Ala Ser Gly Glu Asn Pro Arg Pro
 370 375 380
 Phe Ala Ile Ser Pro Met Pro Asp Phe Gly His Pro Asp Lys Leu Leu
 385 390 395 400
 Val Glu Gly His Glu Ile Pro Leu Val Ser Gln Glu Lys Thr Ile Glu
 30 405 410 415
 Leu Ala Asp Gly Arg Lys Met Thr Val Ser Ala Cys Cys Asp Phe Leu
 420 425 430
 Thr Tyr Val Lys Leu Gly Arg Ile Lys Thr Glu Arg Pro Ala Ala Lys
 435 440 445
 35 Pro Lys Ala Gln Asp Glu Glu Asp Ser Asp Ile Asp Asn Gly Glu Glu
 450 455 460

Ser Glu Asp Glu Ile Gly Asp Glu Glu Glu Gly Thr Glu Asp Ala Ala
 465 470 475 480
 Ala Gly Asp Glu Gly Ser Glu Glu Asp Glu Ala Thr Glu Asn Glu Asp
 485 490 495
 5 Gly Glu Glu Asp Glu Ala Glu Glu Pro Glu Glu Glu Ser Ser Ala Glu
 500 505 510
 Gly Asn Gly Ser Ser Asn Ala Ile Leu Pro Val Pro Glu Ala Ser Lys
 515 520 525
 Gly Arg Asp Ile Asp Leu Phe Leu Lys Gly Ile Arg Thr Ala Glu Thr
 10 530 535 540
 Asn Ile Pro Gln Thr Gly Glu Ala Arg Tyr Thr Gly Thr Trp Glu Ala
 545 550 555 560
 Arg Ile Gly Lys Pro Ile Gln Trp Asp Asn His Ala Asp Lys Glu Ala
 565 570 575
 15 Ala Lys Ala Val Phe Thr Val Asp Phe Gly Lys Lys Ser Ile Ser Gly
 580 585 590
 Thr Leu Thr Glu Lys Asn Gly Val Glu Pro Ala Phe Arg Ile Glu Asn
 595 600 605
 Gly Val Ile Glu Gly Asn Gly Phe His Ala Thr Ala Arg Thr Arg Asp
 20 610 615 620
 Asp Gly Ile Asp Leu Ser Gly Gln Gly Ser Thr Lys Pro Gln Ile Phe
 625 630 635 640
 Lys Ala Asn Asp Leu Arg Val Glu Gly Gly Phe Tyr Gly Pro Lys Ala
 645 650 655
 25 Glu Glu Leu Gly Gly Ile Ile Phe Asn Asn Asp Gly Lys Ser Leu Gly
 660 665 670
 Ile Thr Glu Gly Thr Glu Asn Lys Val Glu Ala Asp Val Asp Val Asp
 675 680 685
 Val Asp Val Asp Val Asp Ala Asp Ala Asp Val Glu Gln Leu Lys Pro
 30 690 695 700
 Glu Val Lys Pro Gln Phe Gly Val Val Phe Gly Ala Lys Lys Asp Asn
 705 710 715 720
 Lys Glu Val Glu Lys
 725

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 2169 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

10 (vi) ORIGINAL SOURCE:

(B) STRAIN: *Neisseria meningitidis* strain M981

(ix) FEATURE:

- 15 (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...2166
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

| | | |
|----|---|-----|
| 20 | ATG TGT AAA CCG AAT TAT GGC GGC ATT GTC TTG TTG CCC TTA CTT TTG | 48 |
| | Met Cys Lys Pro Asn Tyr Gly Gly Ile Val Leu Leu Pro Leu Leu Leu | |
| | 1 5 10 15 | |
| 25 | GCA TCT TGC ATC GGC GGC AAT TTC GGC GTG CAG CCT GTT GTC GAA TCA | 96 |
| | Ala Ser Cys Ile Gly Gly Asn Phe Gly Val Gln Pro Val Val Glu Ser | |
| | 20 25 30 | |
| 30 | ACG CCG ACC GCG TAC CCC GTC ACT TTC AAG TCT AAG GAC GTT CCC ACT | 144 |
| | Thr Pro Thr Ala Tyr Pro Val Thr Phe Lys Ser Lys Asp Val Pro Thr | |
| | 35 40 45 | |
| 35 | TCG CCC CCT GCC GGG TCT TCG GTA GAA ACC ACG CCG GTC AAC CAG CCC | 192 |
| | Ser Pro Pro Ala Gly Ser Ser Val Glu Thr Thr Pro Val Asn Gln Pro | |
| | 50 55 60 | |
| 40 | GCC GTC GGT GCG GCA ATG CGG CTG TTG AGA CGG AAT ACT GCT TTT CAT | 240 |
| | Ala Val Gly Ala Ala Met Arg Leu Leu Arg Arg Asn Thr Ala Phe His | |
| | 65 70 75 80 | |
| 40 | CGT GAA GAT GGC ACG GCA ATT CCC GAT AGC AAA CAA GCA GAA GAA AAG | 288 |
| | Arg Glu Asp Gly Thr Ala Ile Pro Asp Ser Lys Gln Ala Glu Glu Lys | |
| | 85 90 95 | |

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|----|---|-----|
| | CTG TCG TTT AAA GAA GGT GAT GTT CTG TTT TTA TAC GGT TCA AAA GAA | 336 |
| | Leu Ser Phe Lys Glu Gly Asp Val Leu Phe Leu Tyr Gly Ser Lys Glu | |
| | 100 105 110 | |
| 5 | AAT AAA CTT CAA CAA CTT AAA AGC GAA ATT CAT AAA CGT AAT CCT GAG | 384 |
| | Asn Lys Leu Gln Gln Leu Lys Ser Glu Ile His Lys Arg Asn Pro Glu | |
| | 115 120 125 | |
| 10 | GCA AGC ATT ACC ACA TCG GAA AAT GAA AAT AAA AAA TAT AAT TAT CGG | 432 |
| | Ala Ser Ile Thr Thr Ser Glu Asn Glu Asn Lys Lys Tyr Asn Tyr Arg | |
| | 130 135 140 | |
| | TTT GTC AGT GCC GGT TAT GTG TTT ACT AAA AAC GGA AAA GAT GAA ATT | 480 |
| | Phe Val Ser Ala Gly Tyr Val Phe Thr Lys Asn Gly Lys Asp Glu Ile | |
| 15 | 145 150 155 160 | |
| | GAG AAA ACA TCG GAT GAA AAG CAG TTT TCT AAT CGT TTA GGC TAT GAC | 528 |
| | Glu Lys Thr Ser Asp Glu Lys Gln Phe Ser Asn Arg Leu Gly Tyr Asp | |
| | 165 170 175 | |
| 20 | GGT TTT GTA TAT TAT CTC GGA GAA CAT CCT TCC CAA TCT TTA CCG AGC | 576 |
| | Gly Phe Val Tyr Tyr Leu Gly Glu His Pro Ser Gln Ser Leu Pro Ser | |
| | 180 185 190 | |
| 25 | GCG GGA ACG GTG AAA TAT TCC GGC AAC TGG CAA TAT ATG ACC GAT GCC | 624 |
| | Ala Gly Thr Val Lys Tyr Ser Gly Asn Trp Gln Tyr Met Thr Asp Ala | |
| | 195 200 205 | |
| 30 | ATA CGT CAT CGG AGA GGT AAG GGG GTT TCC AGT GTG GAT TTG GGT TAT | 672 |
| | Ile Arg His Arg Arg Gly Lys Gly Val Ser Ser Val Asp Leu Gly Tyr | |
| | 210 215 220 | |
| | ACC ACA TAT TAT GGT AAT GAA ATT GGG GCA GCT TCT TAT GAG GCT AGG | 720 |
| | Thr Thr Tyr Tyr Gly Asn Glu Ile Gly Ala Ala Ser Tyr Glu Ala Arg | |
| 35 | 225 230 235 240 | |
| | GAT GCC GAT GGC CGG GAA AAA CAT CCT GCC GAA TAT ACG GTT AAT TTC | 768 |
| | Asp Ala Asp Gly Arg Glu Lys His Pro Ala Glu Tyr Thr Val Asn Phe | |
| | 245 250 255 | |
| 40 | GAC AAA AAA AAC CTG GAA GGT AAG TTG ATT AAA AAT CAG TAT GTG CAA | 816 |
| | Asp Lys Lys Asn Leu Glu Gly Lys Leu Ile Lys Asn Gln Tyr Val Gln | |
| | 260 265 270 | |

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|----|---|------|
| | AAG AGA GAT GAT CCT AAA AAT CCA CTG ACC ATT TAC AAC ATT ACC GCA | 864 |
| | Lys Arg Asp Asp Pro Lys Asn Pro Leu Thr Ile Tyr Asn Ile Thr Ala | |
| | 275 280 285 | |
| 5 | ACA TTG GAC GGC AAC CGC TTT ACC GGC AGT GCC AAA GTT AGC ACC GAG | 912 |
| | Thr Leu Asp Gly Asn Arg Phe Thr Gly Ser Ala Lys Val Ser Thr Glu | |
| | 290 295 300 | |
| 10 | GTG AAG ACG CAA CAC GCT GAT AAA GAA TAT TTG TTT TTC CAT ACC GAT | 960 |
| | Val Lys Thr Gln His Ala Asp Lys Glu Tyr Leu Phe Phe His Thr Asp | |
| | 305 310 315 320 | |
| 15 | GCC GAT CAG CGG CTT GAG GGC GGT TTT TTC GGC GAT AAC GGA GAA GAG | 1008 |
| | Ala Asp Gln Arg Leu Glu Gly Gly Phe Phe Gly Asp Asn Gly Glu Glu | |
| | 325 330 335 | |
| 20 | CTT GCC GGG CGG TTT ATC AGT AAC GAC AAC AGC GTA TTC GGC GTG TTC | 1056 |
| | Leu Ala Gly Arg Phe Ile Ser Asn Asp Asn Ser Val Phe Gly Val Phe | |
| | 340 345 350 | |
| 25 | GCA GGC AAA CAA AAA ACA GAG ACA GCA AAC GCA TCA GAT ACA AAT CCT | 1104 |
| | Ala Gly Lys Gln Lys Thr Glu Thr Ala Asn Ala Ser Asp Thr Asn Pro | |
| | 355 360 365 | |
| 30 | GCC CTG CCG TCT GGA AAA CAC ACC AAA ATC TTG GAT TCT CTA AAA ATT | 1152 |
| | Ala Leu Pro Ser Gly Lys His Thr Lys Ile Leu Asp Ser Leu Lys Ile | |
| | 370 375 380 | |
| 35 | TCC GTT GAC GAG GCG ACT GAT GAC CAT GCC CGT AAG TTT GCC ATT TCC | 1200 |
| | Ser Val Asp Glu Ala Thr Asp Asp His Ala Arg Lys Phe Ala Ile Ser | |
| | 385 390 395 400 | |
| 40 | ACT ATG CCC GAT TTT GGT CAT CCC GAC AAA CTT CTT GTC GAA GGG CGT | 1248 |
| | Thr Met Pro Asp Phe Gly His Pro Asp Lys Leu Leu Val Glu Gly Arg | |
| | 405 410 415 | |
| 45 | GAA ATT CCT TTG GTT AGC CAA GAG AAA ACC ATC GAG CTT GCC GAC GGC | 1296 |
| | Glu Ile Pro Leu Val Ser Gln Glu Lys Thr Ile Glu Leu Ala Asp Gly | |
| | 420 425 430 | |

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|----|---|------|
| | AGG AAA ATG ACC ATC CGT GCT TGT TGC GAT TTT CTG ACC TAT GTG AAA | 1344 |
| | Arg Lys Met Thr Ile Arg Ala Cys Cys Asp Phe Leu Thr Tyr Val Lys | |
| | 435 440 445 | |
| 5 | CTC GGA CGG ATA AAA ACC GAC CGC CCC GCC GTC AAA CCG AAG GCG CAG | 1392 |
| | Leu Gly Arg Ile Lys Thr Asp Arg Pro Ala Val Lys Pro Lys Ala Gln | |
| | 450 455 460 | |
| 10 | GAT GAA GAG GAT TCG GAC ATT GAT AAT GGC GAA GAA AGC GAA GAC GAA | 1440 |
| | Asp Glu Glu Asp Ser Asp Ile Asp Asn Gly Glu Glu Ser Glu Asp Glu | |
| | 465 470 475 480 | |
| 15 | ATT TCC GAA GAT GAT AAC GGC GAA GAT GAA GTC ACC GAA GAA GAG GAA | 1488 |
| | Ile Ser Glu Asp Asp Asn Gly Glu Asp Glu Val Thr Glu Glu Glu Glu | |
| | 485 490 495 | |
| 20 | GCT GAA GAA ACC GAA GAA GAA ACT GAT GAA GAC GAA GAG GAA GAA CCC | 1536 |
| | Ala Glu Glu Thr Glu Glu Glu Thr Asp Glu Asp Glu Glu Glu Glu Pro | |
| | 500 505 510 | |
| 25 | GAA GAA ACT GAA GAA ACT GAA GAA ACT GAA GAA ACT GAA GAA ACT GAA | 1584 |
| | Glu Glu Thr Glu Glu Thr Glu Glu Thr Glu Glu Thr Glu Glu Thr Glu | |
| | 515 520 525 | |
| 30 | GAA ACT GAA GAA AAA TCG CCG ACA GAA GAA GGC AAC GGC GGT TCA GGC | 1632 |
| | Glu Thr Glu Glu Lys Ser Pro Thr Glu Glu Gly Asn Gly Gly Ser Gly | |
| | 530 535 540 | |
| 35 | AGC ATC CTG CCC ACT CCG GAA GCC TCT AAA GGC AGG GAC ATC GAC CTT | 1680 |
| | Ser Ile Leu Pro Thr Pro Glu Ala Ser Lys Gly Arg Asp Ile Asp Leu | |
| | 545 550 555 560 | |
| 40 | TTC CTG AAA GGT ATC CGC ACG GCG GAA GCC GAC ATT CCG CAA ATT GGA | 1728 |
| | Phe Leu Lys Gly Ile Arg Thr Ala Glu Ala Asp Ile Pro Gln Ile Gly | |
| | 565 570 575 | |
| 45 | AAA GCA CGC TAT ACC GGC ACT TGG GAA GCG CGT ATC GGC GTG CCG GAT | 1776 |
| | Lys Ala Arg Tyr Thr Gly Thr Trp Glu Ala Arg Ile Gly Val Pro Asp | |
| | 580 585 590 | |
| 50 | AAG AAA GGC GAA CAG CTA GAT GGC ACT ACG TCC ATT CAA AAG GAT AGC | 1824 |
| | Lys Lys Gly Glu Gln Leu Asp Gly Thr Thr Ser Ile Gln Lys Asp Ser | |
| | 595 600 605 | |

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|----|---|------|
| | TAT GCG AAT CAA GCG GCA AAA GCA GAA TTT GAC GTT GAT TTT GGT GCG | 1872 |
| | Tyr Ala Asn Gln Ala Ala Lys Ala Glu Phe Asp Val Asp Phe Gly Ala | |
| | 610 615 620 | |
| 5 | AAG TCG CTT TCA GGT AAG TTG ACA GAA AAA AAT GAT ACA CAC CCC GCT | 1920 |
| | Lys Ser Leu Ser Gly Lys Leu Thr Glu Lys Asn Asp Thr His Pro Ala | |
| | 625 630 635 640 | |
| 10 | TTT TAT ATT GAA AAA GGT GTG ATT GAT GGC AAC GGT TTC CAC GCT TTG | 1968 |
| | Phe Tyr Ile Glu Lys Gly Val Ile Asp Gly Asn Gly Phe His Ala Leu | |
| | 645 650 655 | |
| | GCG CGT ACT CGT GAA AAT GGT GTT GAT TTG TCT GGG CAA GGT TCG ACT | 2016 |
| 15 | Ala Arg Thr Arg Glu Asn Gly Val Asp Leu Ser Gly Gln Gly Ser Thr | |
| | 660 665 670 | |
| | AAT CCC CAA AGT TTT AAA GCC AGT AAT CTT CTC GTA GAA GGA GGA TTT | 2064 |
| | Asn Pro Gln Ser Phe Lys Ala Ser Asn Leu Leu Val Glu Gly Gly Phe | |
| 20 | 675 680 685 | |
| | TAT GGT CCG CAG GCG GCA GAG TTG GGT GGT AAT ATT ATC GAC AGT GAC | 2112 |
| | Tyr Gly Pro Gln Ala Ala Glu Leu Gly Gly Asn Ile Ile Asp Ser Asp | |
| | 690 695 700 | |
| 25 | CGG AAA ATC GGC GTG GTA TTC GGT GCG AAG AAA GAT ATG CAG GAG GTG | 2160 |
| | Arg Lys Ile Gly Val Val Phe Gly Ala Lys Lys Asp Met Gln Glu Val | |
| | 705 710 715 720 | |
| 30 | GAA AAA TGA | 2169 |
| | Glu Lys | |

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 722 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(B) STRAIN: Neisseria meningitidis strain M981

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

15 Met Cys Lys Pro Asn Tyr Gly Gly Ile Val Leu Leu Pro Leu Leu Leu
 1 5 10 15
 Ala Ser Cys Ile Gly Gly Asn Phe Gly Val Gln Pro Val Val Glu Ser
 20 20 25 30
 Thr Pro Thr Ala Tyr Pro Val Thr Phe Lys Ser Lys Asp Val Pro Thr
 35 40 45
 Ser Pro Pro Ala Gly Ser Ser Val Glu Thr Thr Pro Val Asn Gln Pro
 50 55 60
 Ala Val Gly Ala Ala Met Arg Leu Leu Arg Arg Asn Thr Ala Phe His
 25 65 70 75 80
 Arg Glu Asp Gly Thr Ala Ile Pro Asp Ser Lys Gln Ala Glu Glu Lys
 85 90 95
 Leu Ser Phe Lys Glu Gly Asp Val Leu Phe Leu Tyr Gly Ser Lys Glu
 100 105 110
 30 Asn Lys Leu Gln Gln Leu Lys Ser Glu Ile His Lys Arg Asn Pro Glu
 115 120 125
 Ala Ser Ile Thr Thr Ser Glu Asn Glu Asn Lys Lys Tyr Asn Tyr Arg
 130 135 140
 Phe Val Ser Ala Gly Tyr Val Phe Thr Lys Asn Gly Lys Asp Glu Ile
 35 145 150 155 160
 Glu Lys Thr Ser Asp Glu Lys Gln Phe Ser Asn Arg Leu Gly Tyr Asp
 165 170 175
 Gly Phe Val Tyr Tyr Leu Gly Glu His Pro Ser Gln Ser Leu Pro Ser
 180 185 190
 40 Ala Gly Thr Val Lys Tyr Ser Gly Asn Trp Gln Tyr Met Thr Asp Ala
 195 200 205
 Ile Arg His Arg Arg Gly Lys Gly Val Ser Ser Val Asp Leu Gly Tyr
 210 215 220

16

Thr Thr Tyr Tyr Gly Asn Glu Ile Gly Ala Ala Ser Tyr Glu Ala Arg
 225 230 235 240
 Asp Ala Asp Gly Arg Glu Lys His Pro Ala Glu Tyr Thr Val Asn Phe
 245 250 255
 5 Asp Lys Lys Asn Leu Glu Gly Lys Leu Ile Lys Asn Gln Tyr Val Gln
 260 265 270
 Lys Arg Asp Asp Pro Lys Asn Pro Leu Thr Ile Tyr Asn Ile Thr Ala
 275 280 285
 Thr Leu Asp Gly Asn Arg Phe Thr Gly Ser Ala Lys Val Ser Thr Glu
 10 290 295 300
 Val Lys Thr Gln His Ala Asp Lys Glu Tyr Leu Phe Phe His Thr Asp
 305 310 315 320
 Ala Asp Gln Arg Leu Glu Gly Gly Phe Phe Gly Asp Asn Gly Glu Glu
 325 330 335
 15 Leu Ala Gly Arg Phe Ile Ser Asn Asp Asn Ser Val Phe Gly Val Phe
 340 345 350
 Ala Gly Lys Gln Lys Thr Glu Thr Ala Asn Ala Ser Asp Thr Asn Pro
 355 360 365
 Ala Leu Pro Ser Gly Lys His Thr Lys Ile Leu Asp Ser Leu Lys Ile
 20 370 375 380
 Ser Val Asp Glu Ala Thr Asp Asp His Ala Arg Lys Phe Ala Ile Ser
 385 390 395 400
 Thr Met Pro Asp Phe Gly His Pro Asp Lys Leu Leu Val Glu Gly Arg
 405 410 415
 25 Glu Ile Pro Leu Val Ser Gln Glu Lys Thr Ile Glu Leu Ala Asp Gly
 420 425 430
 Arg Lys Met Thr Ile Arg Ala Cys Cys Asp Phe Leu Thr Tyr Val Lys
 435 440 445
 Leu Gly Arg Ile Lys Thr Asp Arg Pro Ala Val Lys Pro Lys Ala Gln
 30 450 455 460
 Asp Glu Glu Asp Ser Asp Ile Asp Asn Gly Glu Glu Ser Glu Asp Glu
 465 470 475 480
 Ile Ser Glu Asp Asp Asn Gly Glu Asp Glu Val Thr Glu Glu Glu Glu
 485 490 495
 35 Ala Glu Glu Thr Glu Glu Glu Thr Asp Glu Asp Glu Glu Glu Glu Pro
 500 505 510
 Glu Glu Thr Glu Glu Thr Glu Glu Thr Glu Glu Thr Glu Glu Thr Glu
 515 520 525
 Glu Thr Glu Glu Lys Ser Pro Thr Glu Glu Gly Asn Gly Gly Ser Gly
 40 530 535 540
 Ser Ile Leu Pro Thr Pro Glu Ala Ser Lys Gly Arg Asp Ile Asp Leu
 545 550 555 560

[illegible]

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|----|---|-----|
| | GAA AAG CTG TCG TTT AAA GAA GGT GAT GTT CTG TTT TTA TAC GGT TCA | 336 |
| | Glu Lys Leu Ser Phe Lys Glu Gly Asp Val Leu Phe Leu Tyr Gly Ser | |
| | 100 105 110 | |
| 5 | AAA AAA GAT AAA CTT CAG TGG CTT AAG GAT AAA ATT CAT CAA CGC AAT | 384 |
| | Lys Lys Asp Lys Leu Gln Trp Leu Lys Asp Lys Ile His Gln Arg Asn | |
| | 115 120 125 | |
| 10 | CCT AAT GTA GAA ATT AGG ACA TCA GAA AAT GAA AAT AAA AAA TAT GGT | 432 |
| | Pro Asn Val Glu Ile Arg Thr Ser Glu Asn Glu Asn Lys Lys Tyr Gly | |
| | 130 135 140 | |
| | TAT GAA TTT GTG GAT GCC GGT TAT GTA TAT ACT AAA AAC GGA ACA GAT | 480 |
| | Tyr Glu Phe Val Asp Ala Gly Tyr Val Tyr Thr Lys Asn Gly Thr Asp | |
| 15 | 145 150 155 160 | |
| | GAA ATT GAG TGG ACT TCA AAT CGC AAG CAG TTT TCT AAT CGT TTT GGC | 528 |
| | Glu Ile Glu Trp Thr Ser Asn Arg Lys Gln Phe Ser Asn Arg Phe Gly | |
| | 165 170 175 | |
| 20 | TAC GAC GGT TTT GTA TAT TAT TCC GGA GAA CAT CCT TCC CAA TCT TTA | 576 |
| | Tyr Asp Gly Phe Val Tyr Tyr Ser Gly Glu His Pro Ser Gln Ser Leu | |
| | 180 185 190 | |
| 25 | CCG AGC GCG GGA ACG GTG CAA TAT TCC GGT AAC TGG CAA TAT ATG ACC | 624 |
| | Pro Ser Ala Gly Thr Val Gln Tyr Ser Gly Asn Trp Gln Tyr Met Thr | |
| | 195 200 205 | |
| 30 | GAT GCC ATA CGT CAT CGA ACA GGA AAA GCA GGA GAT CCT AGC GAA GAT | 672 |
| | Asp Ala Ile Arg His Arg Thr Gly Lys Ala Gly Asp Pro Ser Glu Asp | |
| | 210 215 220 | |
| | TTG GGT TAT CTC GTT TAT TAC GGT CAA AAT GTC GGA GCA ACT TCT TAT | 720 |
| | Leu Gly Tyr Leu Val Tyr Tyr Gly Gln Asn Val Gly Ala Thr Ser Tyr | |
| 35 | 225 230 235 240 | |
| | GCT GCG ACT GCC GAC GAC CGG GAG GGA AAA CAT CCT GCC GAA TAT ACG | 768 |
| | Ala Ala Thr Ala Asp Asp Arg Glu Gly Lys His Pro Ala Glu Tyr Thr | |
| | 245 250 255 | |
| 40 | GTT GAT TTC GAT AAG AAA ACT TTG ACG GGT CAA TTA ATT AAA AAT CAG | 816 |
| | Val Asp Phe Asp Lys Lys Thr Leu Thr Gly Gln Leu Ile Lys Asn Gln | |
| | 260 265 270 | |

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|----|---|------|
| | TAT GTG CAA AAG AAA ACC GAT GAA AAG AAA CCA CTG ACC ATT TAC GAC | 864 |
| | Tyr Val Gln Lys Lys Thr Asp Glu Lys Lys Pro Leu Thr Ile Tyr Asp | |
| | 275 280 285 | |
| 5 | ATT ACC GCA ACA TTG GAC GGC AAC CGC TTT ACC GGC AGT GCC AAA GTT | 912 |
| | Ile Thr Ala Thr Leu Asp Gly Asn Arg Phe Thr Gly Ser Ala Lys Val | |
| | 290 295 300 | |
| 10 | AAC ACC GAG TTG AAG ACG AGC CAC GCT GAT AAA GAG CAT TTG TTT TTC | 960 |
| | Asn Thr Glu Leu Lys Thr Ser His Ala Asp Lys Glu His Leu Phe Phe | |
| | 305 310 315 320 | |
| 15 | CAT ACC GAT GCC GAT CAG CGG CTT GAG GGC GGT TTT TTC GGC GAT AAG | 1008 |
| | His Thr Asp Ala Asp Gln Arg Leu Glu Gly Gly Phe Phe Gly Asp Lys | |
| | 325 330 335 | |
| 20 | GGG GAA GAG CTT GCC GGA CGG TTT ATC AGC AAC GAC AAC AGC GTA TTC | 1056 |
| | Gly Glu Glu Leu Ala Gly Arg Phe Ile Ser Asn Asp Asn Ser Val Phe | |
| | 340 345 350 | |
| 25 | GGC GTA TTC GCA GGC AAA AAA ACA AAC GCA TCA AAC GCA GCA GAT ACA | 1104 |
| | Gly Val Phe Ala Gly Lys Lys Thr Asn Ala Ser Asn Ala Ala Asp Thr | |
| | 355 360 365 | |
| 30 | AAT CCT GCT ATG CCG TCT GAA AAA CAC ACC AAA ATC TTG GAT TCT CTG | 1152 |
| | Asn Pro Ala Met Pro Ser Glu Lys His Thr Lys Ile Leu Asp Ser Leu | |
| | 370 375 380 | |
| 35 | AAA ATT TCC GTT GAC GAG GCG ACG GAT AAA AAT GCC CGC CCG TTT GCC | 1200 |
| | Lys Ile Ser Val Asp Glu Ala Thr Asp Lys Asn Ala Arg Pro Phe Ala | |
| | 385 390 395 400 | |
| 40 | ATT TCC CCT CTG CCC GAT TTT GGC CAT CCC GAC AAA CTC CTT GTC GAA | 1248 |
| | Ile Ser Pro Leu Pro Asp Phe Gly His Pro Asp Lys Leu Leu Val Glu | |
| | 405 410 415 | |
| 40 | GGG CGT GAA ATT CCT TTG GTT AGC CAA GAG AAA ACC ATC GAG CTT GCC | 1296 |
| | Gly Arg Glu Ile Pro Leu Val Ser Gln Glu Lys Thr Ile Glu Leu Ala | |
| | 420 425 430 | |

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|----|---|------|
| | GAC GGC AGG AAA ATG ACC GTC CGT GCT TGT TGC GAT TTT CTG ACC TAT | 1344 |
| | Asp Gly Arg Lys Met Thr Val Arg Ala Cys Cys Asp Phe Leu Thr Tyr | |
| | 435 440 445 | |
| 5 | GTG AAA CTC GGA CGG ATA AAA ACT GAC CGC CCA GCA AGT AAA CCA AAG | 1392 |
| | Val Lys Leu Gly Arg Ile Lys Thr Asp Arg Pro Ala Ser Lys Pro Lys | |
| | 450 455 460 | |
| 10 | GCG GAA GAT AAA GGG AAG GAT GAA GAG GAT ACA GGC GTT GGT AAC GAC | 1440 |
| | Ala Glu Asp Lys Gly Lys Asp Glu Glu Asp Thr Gly Val Gly Asn Asp | |
| | 465 470 475 480 | |
| 15 | GAA GAA GGC ACG GAA GAT GAA GCC GCA GAA GGC AGC GAA GGA GGC GAA | 1488 |
| | Glu Glu Gly Thr Glu Asp Glu Ala Ala Glu Gly Ser Glu Gly Gly Glu | |
| | 485 490 495 | |
| 20 | GAC GAA ATC GGC GAT GAA GGA GGA GGT GCG GAA GAC GAA GCC GCA GAA | 1536 |
| | Asp Glu Ile Gly Asp Glu Gly Gly Gly Ala Glu Asp Glu Ala Ala Glu | |
| | 500 505 510 | |
| 25 | AAC GAA GGC GGC GAA GAA GAC GAA GCT GAA GAA CCT GAA GAA CCC GAA | 1584 |
| | Asn Glu Gly Gly Glu Glu Asp Glu Ala Glu Glu Pro Glu Glu Pro Glu | |
| | 515 520 525 | |
| 30 | GAA GAA TCG CCG GCA GAA GGC GGC GGT GGT GGT TCA GAC GGC ATC CTG | 1632 |
| | Glu Glu Ser Pro Ala Glu Gly Gly Gly Gly Gly Ser Asp Gly Ile Leu | |
| | 530 535 540 | |
| 35 | CCC GCT CCG GAA GCT CCT AAA GGC AGG GAT ATC GAC CTT TTC CTG AAA | 1680 |
| | Pro Ala Pro Glu Ala Pro Lys Gly Arg Asp Ile Asp Leu Phe Leu Lys | |
| | 545 550 555 560 | |
| 40 | GGT ATC CGC ACG GCG GAA GCC GAC ATT CCG CAA ACT GGA AAA GCA CGC | 1728 |
| | Gly Ile Arg Thr Ala Glu Ala Asp Ile Pro Gln Thr Gly Lys Ala Arg | |
| | 565 570 575 | |
| 45 | TAT ACC GGC ACT TGG GAA GCG CGT ATC AGC AAA CCC ATT CAA TGG GAC | 1776 |
| | Tyr Thr Gly Thr Trp Glu Ala Arg Ile Ser Lys Pro Ile Gln Trp Asp | |
| | 580 585 590 | |
| 50 | AAT CAT GCG GAT AAA AAA GCG GCA AAA GCA GAA TTT GAC GTT GAT TTC | 1824 |
| | Asn His Ala Asp Lys Lys Ala Ala Lys Ala Glu Phe Asp Val Asp Phe | |
| | 595 600 605 | |

| | | |
|----|---|------|
| | GGC GAG AAA TCG ATT TCC GGA ACG CTG ACG GAG AAA AAC GGT GTA CAA | 1872 |
| | Gly Glu Lys Ser Ile Ser Gly Thr Leu Thr Glu Lys Asn Gly Val Gln | |
| | 610 615 620 | |
| 5 | CCT GCT TTC CAT ATT GAA AAC GGC GTG ATT GAG GGC AAT GGT TTC CAC | 1920 |
| | Pro Ala Phe His Ile Glu Asn Gly Val Ile Glu Gly Asn Gly Phe His | |
| | 625 630 635 640 | |
| 10 | GCG ACA GCG CGC ACT CGG GAT AAC GGC ATC AAT CTT TCG GGA AAT GAT | 1968 |
| | Ala Thr Ala Arg Thr Arg Asp Asn Gly Ile Asn Leu Ser Gly Asn Asp | |
| | 645 650 655 | |
| | TCG ACT AAT CCT CCA AGT TTC AAA GCC AAT AAT CTT CTT GTA ACA GGC | 2016 |
| 15 | Ser Thr Asn Pro Pro Ser Phe Lys Ala Asn Asn Leu Leu Val Thr Gly | |
| | 660 665 670 | |
| | GGC TTT TAC GGC CCG CAG GCG GAG GAA TTG GGC GGT ACT ATT TTC AAT | 2064 |
| | Gly Phe Tyr Gly Pro Gln Ala Glu Glu Leu Gly Gly Thr Ile Phe Asn | |
| 20 | 675 680 685 | |
| | AAT GAT GGG AAA TCT CTT GGT ATA ACT GAA GAT ACT GAA AAT GAA GCT | 2112 |
| | Asn Asp Gly Lys Ser Leu Gly Ile Thr Glu Asp Thr Glu Asn Glu Ala | |
| | 690 695 700 | |
| 25 | GAA GCT GAA GTT GAA AAT GAA GCT GGT GTT GGC GAA CAG TTA AAA CCT | 2160 |
| | Glu Ala Glu Val Glu Asn Glu Ala Gly Val Gly Glu Gln Leu Lys Pro | |
| | 705 710 715 720 | |
| 30 | GAA GCT AAA CCC CAA TTC GGC GTG GTA TTC GGT GCG AAG AAA GAT AAT | 2208 |
| | Glu Ala Lys Pro Gln Phe Gly Val Val Phe Gly Ala Lys Lys Asp Asn | |
| | 725 730 735 | |
| | AAA GAG GTG GAA AAA TGA | 2226 |
| 35 | Lys Glu Val Glu Lys | |
| | 740 | |

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 741 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(B) STRAIN: *Neisseria meningitidis* strain H44/76

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

15 Met Cys Lys Pro Asn Tyr Gly Gly Ile Val Leu Leu Pro Leu Leu Leu
 1 5 10 15
 Ala Ser Cys Ile Gly Gly Asn Phe Gly Val Gln Pro Val Val Glu Ser
 20 20 25 30
 Thr Pro Thr Ala Tyr Pro Val Thr Phe Lys Ser Lys Asp Val Pro Thr
 35 40 45
 Pro Pro Pro Ala Lys Pro Ser Ile Glu Thr Thr Pro Val Pro Ser Thr
 50 55 60
 Gly Pro Ala Val Gly Ala Ala Met Arg Leu Leu Arg Arg Ile Phe Ala
 25 65 70 75 80
 Thr Ser Asp Lys Val Gly Asn Asp Phe Pro Asn Ser Lys Gln Ala Glu
 85 90 95
 Glu Lys Leu Ser Phe Lys Glu Gly Asp Val Leu Phe Leu Tyr Gly Ser
 100 105 110
 Lys Lys Asp Lys Leu Gln Trp Leu Lys Asp Lys Ile His Gln Arg Asn
 30 115 120 125
 Pro Asn Val Glu Ile Arg Thr Ser Glu Asn Glu Asn Lys Lys Tyr Gly
 130 135 140
 Tyr Glu Phe Val Asp Ala Gly Tyr Val Tyr Thr Lys Asn Gly Thr Asp
 35 145 150 155 160
 Glu Ile Glu Trp Thr Ser Asn Arg Lys Gln Phe Ser Asn Arg Phe Gly
 165 170 175
 Tyr Asp Gly Phe Val Tyr Tyr Ser Gly Glu His Pro Ser Gln Ser Leu
 180 185 190
 40 Pro Ser Ala Gly Thr Val Gln Tyr Ser Gly Asn Trp Gln Tyr Met Thr
 195 200 205
 Asp Ala Ile Arg His Arg Thr Gly Lys Ala Gly Asp Pro Ser Glu Asp
 210 215 220

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|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|
| | | | | | | | | | 24 | | | | | | | | | | |
| | Leu | Gly | Tyr | Leu | Val | Tyr | Tyr | Gly | Gln | Asn | Val | Gly | Ala | Thr | Ser | Tyr | | | |
| | 225 | | | | | | 230 | | | | | 235 | | | | 240 | | | |
| | Ala | Ala | Thr | Ala | Asp | Asp | Arg | Glu | Gly | Lys | His | Pro | Ala | Glu | Tyr | Thr | | | |
| | | | | | 245 | | | | | 250 | | | | | | 255 | | | |
| 5 | Val | Asp | Phe | Asp | Lys | Lys | Thr | Leu | Thr | Gly | Gln | Leu | Ile | Lys | Asn | Gln | | | |
| | | | | 260 | | | | | 265 | | | | | | 270 | | | | |
| | Tyr | Val | Gln | Lys | Lys | Thr | Asp | Glu | Lys | Lys | Pro | Leu | Thr | Ile | Tyr | Asp | | | |
| | | | | 275 | | | | | 280 | | | | | 285 | | | | | |
| | Ile | Thr | Ala | Thr | Leu | Asp | Gly | Asn | Arg | Phe | Thr | Gly | Ser | Ala | Lys | Val | | | |
| 10 | | 290 | | | | | 295 | | | | | 300 | | | | | | | |
| | Asn | Thr | Glu | Leu | Lys | Thr | Ser | His | Ala | Asp | Lys | Glu | His | Leu | Phe | Phe | | | |
| | 305 | | | | | 310 | | | | | | 315 | | | | 320 | | | |
| | His | Thr | Asp | Ala | Asp | Gln | Arg | Leu | Glu | Gly | Gly | Phe | Phe | Gly | Asp | Lys | | | |
| | | | | | 325 | | | | | 330 | | | | | | 335 | | | |
| 15 | Gly | Glu | Glu | Leu | Ala | Gly | Arg | Phe | Ile | Ser | Asn | Asp | Asn | Ser | Val | Phe | | | |
| | | | | 340 | | | | | 345 | | | | | 350 | | | | | |
| | Gly | Val | Phe | Ala | Gly | Lys | Lys | Thr | Asn | Ala | Ser | Asn | Ala | Ala | Asp | Thr | | | |
| | | | | 355 | | | | 360 | | | | | | 365 | | | | | |
| | Asn | Pro | Ala | Met | Pro | Ser | Glu | Lys | His | Thr | Lys | Ile | Leu | Asp | Ser | Leu | | | |
| 20 | | 370 | | | | | 375 | | | | | 380 | | | | | | | |
| | Lys | Ile | Ser | Val | Asp | Glu | Ala | Thr | Asp | Lys | Asn | Ala | Arg | Pro | Phe | Ala | | | |
| | 385 | | | | | 390 | | | | | 395 | | | | | 400 | | | |
| | Ile | Ser | Pro | Leu | Pro | Asp | Phe | Gly | His | Pro | Asp | Lys | Leu | Leu | Val | Glu | | | |
| | | | | | 405 | | | | | 410 | | | | | | 415 | | | |
| 25 | Gly | Arg | Glu | Ile | Pro | Leu | Val | Ser | Gln | Glu | Lys | Thr | Ile | Glu | Leu | Ala | | | |
| | | | | 420 | | | | | 425 | | | | | 430 | | | | | |
| | Asp | Gly | Arg | Lys | Met | Thr | Val | Arg | Ala | Cys | Cys | Asp | Phe | Leu | Thr | Tyr | | | |
| | | | | 435 | | | | 440 | | | | | | 445 | | | | | |
| | Val | Lys | Leu | Gly | Arg | Ile | Lys | Thr | Asp | Arg | Pro | Ala | Ser | Lys | Pro | Lys | | | |
| 30 | | 450 | | | | | 455 | | | | | 460 | | | | | | | |
| | Ala | Glu | Asp | Lys | Gly | Lys | Asp | Glu | Glu | Asp | Thr | Gly | Val | Gly | Asn | Asp | | | |
| | 465 | | | | | 470 | | | | | 475 | | | | | 480 | | | |
| | Glu | Glu | Gly | Thr | Glu | Asp | Glu | Ala | Ala | Glu | Gly | Ser | Glu | Gly | Gly | Glu | | | |
| | | | | | 485 | | | | | 490 | | | | | | 495 | | | |
| 35 | Asp | Glu | Ile | Gly | Asp | Glu | Gly | Gly | Gly | Ala | Glu | Asp | Glu | Ala | Ala | Glu | | | |
| | | | | 500 | | | | | 505 | | | | | 510 | | | | | |
| | Asn | Glu | Gly | Gly | | | | | | | | | | | | | | | |

[illegible]

(2) INFORMATION FOR SEQ ID NO:7:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2262 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: cDNA
(vi) ORIGINAL SOURCE:
(B) STRAIN: Neisseria meningitidis strain M990
(ix) FEATURE:

40 (A) NAME/KEY: Coding Sequence
(B) LOCATION: 1...2259
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

| | | |
|----|---|-----|
| 5 | ATG TGT AAA CCG AAT TAT GGC GGC ATT GTC TTG TTG CCC TTA CTT TTA | 48 |
| | Met Cys Lys Pro Asn Tyr Gly Gly Ile Val Leu Leu Pro Leu Leu Leu | |
| | 1 5 10 15 | |
| 10 | GCA TCT TGT ATC GGC GGC AAT TTC GGC GTA CAG CCT GTT GTC GAA TCA | 96 |
| | Ala Ser Cys Ile Gly Gly Asn Phe Gly Val Gln Pro Val Val Glu Ser | |
| | 20 25 30 | |
| 15 | ACG CCG ACC GCG CCA ACT CTG TCA GAT TCC AAA TCT TCC AAT CCT GCG | 144 |
| | Thr Pro Thr Ala Pro Thr Leu Ser Asp Ser Lys Ser Ser Asn Pro Ala | |
| | 35 40 45 | |
| 20 | GAT AAG CCT GCT CCA GCT CCT GCC GAG CCT TCG GTA GAA ATC ACG CCG | 192 |
| | Asp Lys Pro Ala Pro Ala Pro Ala Glu Pro Ser Val Glu Ile Thr Pro | |
| | 50 55 60 | |
| 25 | GTC AAG CGG CCC GCC GTC GGT GCG GCA ATG CGG CTG CCA AGG CGG AAT | 240 |
| | Val Lys Arg Pro Ala Val Gly Ala Ala Met Arg Leu Pro Arg Arg Asn | |
| | 65 70 75 80 | |
| 30 | ATC GCA ACT TTT GAT AAA AAT GGT AAT GAA ATT CCC AAT AGT AAG CAG | 288 |
| | Ile Ala Thr Phe Asp Lys Asn Gly Asn Glu Ile Pro Asn Ser Lys Gln | |
| | 85 90 95 | |
| 35 | GCA GAG GAG TAT CTG CCG CTC AAA GAG AAG GAT ATC CTG TTT TTA GAC | 336 |
| | Ala Glu Glu Tyr Leu Pro Leu Lys Glu Lys Asp Ile Leu Phe Leu Asp | |
| | 100 105 110 | |
| 40 | GGT ACG CCG AAA GAA CAG GCT GAC AAA CTT AAA AAG GAA ATC AAC GGA | 384 |
| | Gly Thr Pro Lys Glu Gln Ala Asp Lys Leu Lys Lys Glu Ile Asn Gly | |
| | 115 120 125 | |
| 45 | CGG CAT CCT AAT GCA CCA ATC TAC ACG TCC GAT TTA AAA GAT GAT GCG | 432 |
| | Arg His Pro Asn Ala Pro Ile Tyr Thr Ser Asp Leu Lys Asp Asp Ala | |
| | 130 135 140 | |
| 50 | TAT CAA TAT AAA TAT GTC CGG GCC GGA TAT GTT TAT ACT AGA TAT GGA | 480 |
| | Tyr Gln Tyr Lys Tyr Val Arg Ala Gly Tyr Val Tyr Thr Arg Tyr Gly | |
| | 145 150 155 160 | |

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|----|---|------|
| | ACA GAT GAA ATC GAA CAG AAC TCA GGC GGT AAG CGG GTT ACC CAC CGC | 528 |
| | Thr Asp Glu Ile Glu Gln Asn Ser Gly Gly Lys Arg Val Thr His Arg | |
| | 165 170 175 | |
| 5 | TTA GGT TAT GAC GGT TTT GTA TAT TAT TCC GGA GAA CGT CCT TCC CAA | 576 |
| | Leu Gly Tyr Asp Gly Phe Val Tyr Tyr Ser Gly Glu Arg Pro Ser Gln | |
| | 180 185 190 | |
| 10 | TCT TTA CCG AGT GCG GGA ACG GTG GAA TAT TCT GGT AAC TGG CAA TAT | 624 |
| | Ser Leu Pro Ser Ala Gly Thr Val Glu Tyr Ser Gly Asn Trp Gln Tyr | |
| | 195 200 205 | |
| 15 | ATG ACC GAT GCC AAA CGT CAT CGA GCA GGT CAG GCG GTT GGC ATT GAC | 672 |
| | Met Thr Asp Ala Lys Arg His Arg Ala Gly Gln Ala Val Gly Ile Asp | |
| | 210 215 220 | |
| 20 | AAT TTG GGT TAT ATC ACA TTT TAT GGT AAC GAT GTT GGT GCA ACT TCT | 720 |
| | Asn Leu Gly Tyr Ile Thr Phe Tyr Gly Asn Asp Val Gly Ala Thr Ser | |
| | 225 230 235 240 | |
| | TAT GCG GCT AAG GAT GTC GAC GAA AGG GAA AAG CAT CCT GCC AAA TAT | 768 |
| | Tyr Ala Ala Lys Asp Val Asp Glu Arg Glu Lys His Pro Ala Lys Tyr | |
| | 245 250 255 | |
| 25 | ACG GTT GAT TTT GAT AAC AAA ACC ATG AAT GGC AAG CTG ATT AAA AAT | 816 |
| | Thr Val Asp Phe Asp Asn Lys Thr Met Asn Gly Lys Leu Ile Lys Asn | |
| | 260 265 270 | |
| 30 | CAG TAT GTG CGA AAT AAA AAA GAT GAA CCC AAA AAA CCG CTG ACC ATT | 864 |
| | Gln Tyr Val Arg Asn Lys Lys Asp Glu Pro Lys Lys Pro Leu Thr Ile | |
| | 275 280 285 | |
| 35 | TAC GAC ATT ACT GCA AAA TTG GAC GGC AAC CGC TTT ACC GGC AGT GCC | 912 |
| | Tyr Asp Ile Thr Ala Lys Leu Asp Gly Asn Arg Phe Thr Gly Ser Ala | |
| | 290 295 300 | |
| 40 | AAG GTC AAT CCT GAT TTA GCG AAA AAC CTT GCC GGT AAT GAG CGT TTG | 960 |
| | Lys Val Asn Pro Asp Leu Ala Lys Asn Leu Ala Gly Asn Glu Arg Leu | |
| | 305 310 315 320 | |
| | TTT TTC CAT GCC GAT GCC GAT CAG CGG CTT GAG GGC GGT TTT TTC GGC | 1008 |
| | Phe Phe His Ala Asp Ala Asp Gln Arg Leu Glu Gly Gly Phe Phe Gly | |
| | 325 330 335 | |

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|----|---|------|
| | GAT AAC GGA GAA GAG CTT GCC GGA CGG TTT ATC AGC AAC GAC AAC AGC | 1056 |
| | Asp Asn Gly Glu Glu Leu Ala Gly Arg Phe Ile Ser Asn Asp Asn Ser | |
| | 340 345 350 | |
| 5 | GTA TTC GGC GTA TTC GCA GGC AAA AAA ACA GAG ACA GCA AAC GCA GCA | 1104 |
| | Val Phe Gly Val Phe Ala Gly Lys Lys Thr Glu Thr Ala Asn Ala Ala | |
| | 355 360 365 | |
| 10 | GAT ACA AAA CCT GCC CTG CCG TCT GGA AAA CAC ACC AAA ATC TTG GAT | 1152 |
| | Asp Thr Lys Pro Ala Leu Pro Ser Gly Lys His Thr Lys Ile Leu Asp | |
| | 370 375 380 | |
| 15 | TCT CTA AAA ATT TCC GTT GAC GAG GCG ACT GAT GGC CAT GCC CGT AAG | 1200 |
| | Ser Leu Lys Ile Ser Val Asp Glu Ala Thr Asp Gly His Ala Arg Lys | |
| | 385 390 395 400 | |
| 20 | TTT GCC ATT TCC TCT ATG CCC GAT TTT GGT CAT CCC GAC AAA CTT CTT | 1248 |
| | Phe Ala Ile Ser Ser Met Pro Asp Phe Gly His Pro Asp Lys Leu Leu | |
| | 405 410 415 | |
| 25 | GTC GAA GGG CGT GAA ATT CCT TTG GTA AAC GAA GAA CAA ATC ATC AAG | 1296 |
| | Val Glu Gly Arg Glu Ile Pro Leu Val Asn Glu Glu Gln Ile Ile Lys | |
| | 420 425 430 | |
| 30 | CTT GCC GAC GGC AGG AAA ATG ACC GTC CGT GCT TGT TGC GAC TTT TTG | 1344 |
| | Leu Ala Asp Gly Arg Lys Met Thr Val Arg Ala Cys Cys Asp Phe Leu | |
| | 435 440 445 | |
| 35 | ACC TAT GTG AAA CTC GGA CGG ATA AAA ACC GAT CGC CCG GCA AGT AAA | 1392 |
| | Thr Tyr Val Lys Leu Gly Arg Ile Lys Thr Asp Arg Pro Ala Ser Lys | |
| | 450 455 460 | |
| 40 | CCA AAG GCG GAA GAT AAA GGG GAG GAT GAA GAG GGT GCA GGC GTT GAT | 1440 |
| | Pro Lys Ala Glu Asp Lys Gly Glu Asp Glu Glu Gly Ala Gly Val Asp | |
| | 465 470 475 480 | |
| | AAC GAC GAA GAA AGC GAA GAC GAA GCC GTA GAA GAC GAA GGC GGC GAA | 1488 |
| | Asn Asp Glu Glu Ser Glu Asp Glu Ala Val Glu Asp Glu Gly Gly Glu | |
| | 485 490 495 | |

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|----|---|------|
| | GAA GAC GAA ACT TCC GAA GAG GAT AAT GGC GAA GAC GAA GAA GCA ACC | 1536 |
| | Glu Asp Glu Thr Ser Glu Glu Asp Asn Gly Glu Asp Glu Glu Ala Thr | |
| | 500 505 510 | |
| 5 | GCC GAA GAA GAA ACC GAA GAA GTT GAT GAA GCC GAA GAG GAG GAA GTT | 1584 |
| | Ala Glu Glu Glu Thr Glu Glu Val Asp Glu Ala Glu Glu Glu Glu Val | |
| | 515 520 525 | |
| 10 | GAA GAA CCC GAA GAA AAA TCG CCG GCA GAA GGC AAC GGC GGT TCA GGC | 1632 |
| | Glu Glu Pro Glu Glu Lys Ser Pro Ala Glu Gly Asn Gly Gly Ser Gly | |
| | 530 535 540 | |
| 15 | AGC ATC CTG CCT GCC CTA GAA GCC TCT AAA GGC AGG GAC ATC GAC CTT | 1680 |
| | Ser Ile Leu Pro Ala Leu Glu Ala Ser Lys Gly Arg Asp Ile Asp Leu | |
| | 545 550 555 560 | |
| 20 | TTC CTG AAA GGT ATC CGC ACG GCA GAA ACG GAT ATT CCG CAA AGC GGA | 1728 |
| | Phe Leu Lys Gly Ile Arg Thr Ala Glu Thr Asp Ile Pro Gln Ser Gly | |
| | 565 570 575 | |
| 25 | ACG GCG CAT TAT ACC GGC ACT TGG GAA GCG CGT ATC GGC AAA CCC ATT | 1776 |
| | Thr Ala His Tyr Thr Gly Thr Trp Glu Ala Arg Ile Gly Lys Pro Ile | |
| | 580 585 590 | |
| 30 | CAA TGG GAC AAT CAG GCG GAT GAA AAA GCG GCA AAA GCA GAA TTT ACC | 1824 |
| | Gln Trp Asp Asn Gln Ala Asp Glu Lys Ala Ala Lys Ala Glu Phe Thr | |
| | 595 600 605 | |
| 35 | GTT GAT TTC GAC AAG AAA TCG ATT TCC GGA AAG CTG ACG GAG CAA AAC | 1872 |
| | Val Asp Phe Asp Lys Lys Ser Ile Ser Gly Lys Leu Thr Glu Gln Asn | |
| | 610 615 620 | |
| 40 | GGC GTA GAA CCT GCT TTC CAT ATT GAA GAC GGC AAG ATT GAT GGC AAC | 1920 |
| | Gly Val Glu Pro Ala Phe His Ile Glu Asp Gly Lys Ile Asp Gly Asn | |
| | 625 630 635 640 | |
| 45 | GGT TTC CAC GCG ACA GCG CGC ACT CGG GAG AGC GGC ATC AAT CTT TCG | 1968 |
| | Gly Phe His Ala Thr Ala Arg Thr Arg Glu Ser Gly Ile Asn Leu Ser | |
| | 645 650 655 | |
| 50 | GGA AAT GGT TCG ACC GAC CCC AAA ACA TTC CAA GCT AGT AAT CTT CGT | 2016 |
| | Gly Asn Gly Ser Thr Asp Pro Lys Thr Phe Gln Ala Ser Asn Leu Arg | |
| | 660 665 670 | |

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|----|---|------|
| | GTA GAA GGA GGA TTT TAC GGC CCG CAG GCG GCG GAA TTG GGC GGT ACT | 2064 |
| | Val Glu Gly Gly Phe Tyr Gly Pro Gln Ala Ala Glu Leu Gly Gly Thr | |
| | 675 680 685 | |
| 5 | ATT TTC AAT AAT GAT GGG AAA TCT CTT AGT ATA ACT GAA AAT ATT GAA | 2112 |
| | Ile Phe Asn Asn Asp Gly Lys Ser Leu Ser Ile Thr Glu Asn Ile Glu | |
| | 690 695 700 | |
| 10 | AAT GAA GCT GAA GCT GAA GTT GAA GTT GAA GCT GAA GCT GAA GTT GAA | 2160 |
| | Asn Glu Ala Glu Ala Glu Val Glu Val Glu Ala Glu Ala Glu Val Glu | |
| | 705 710 715 720 | |
| 15 | GTT GAA GCT GAT GTT GGC AAA CAG TTA GAA CCT GAT GAA GTT AAA CAC | 2208 |
| | Val Glu Ala Asp Val Gly Lys Gln Leu Glu Pro Asp Glu Val Lys His | |
| | 725 730 735 | |
| 20 | AAA TTC GGC GTG GTA TTC GGT GCG AAG AAA GAT ATG CAG GAG GTG GAA | 2256 |
| | Lys Phe Gly Val Val Phe Gly Ala Lys Lys Asp Met Gln Glu Val Glu | |
| | 740 745 750 | |
| | AAA TGA | 2262 |
| | Lys | |

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(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 753 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(B) STRAIN: *Neisseria meningitidis* strain M990

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Cys Lys Pro Asn Tyr Gly Gly Ile Val Leu Leu Pro Leu Leu Leu
1 5 10 15

31

Ala Ser Cys Ile Gly Gly Asn Phe Gly Val Gln Pro Val Val Glu Ser
 20 25 30

Thr Pro Thr Ala Pro Thr Leu Ser Asp Ser Lys Ser Ser Asn Pro Ala
 35 40 45

5 Asp Lys Pro Ala Pro Ala Pro Ala Glu Pro Ser Val Glu Ile Thr Pro
 50 55 60

Val Lys Arg Pro Ala Val Gly Ala Ala Met Arg Leu Pro Arg Arg Asn
 65 70 75 80

Ile Ala Thr Phe Asp Lys Asn Gly Asn Glu Ile Pro Asn Ser Lys Gln
 85 90 95

10 Ala Glu Glu Tyr Leu Pro Leu Lys Glu Lys Asp Ile Leu Phe Leu Asp
 100 105 110

Gly Thr Pro Lys Glu Gln Ala Asp Lys Leu Lys Lys Glu Ile Asn Gly
 115 120 125

15 Arg His Pro Asn Ala Pro Ile Tyr Thr Ser Asp Leu Lys Asp Asp Ala
 130 135 140

Tyr Gln Tyr Lys Tyr Val Arg Ala Gly Tyr Val Tyr Thr Arg Tyr Gly
 145 150 155 160

Thr Asp Glu Ile Glu Gln Asn Ser Gly Gly Lys Arg Val Thr His Arg
 165 170 175

20 Leu Gly Tyr Asp Gly Phe Val Tyr Tyr Ser Gly Glu Arg Pro Ser Gln
 180 185 190

Ser Leu Pro Ser Ala Gly Thr Val Glu Tyr Ser Gly Asn Trp Gln Tyr
 195 200 205

25 Met Thr Asp Ala Lys Arg His Arg Ala Gly Gln Ala Val Gly Ile Asp
 210 215 220

Asn Leu Gly Tyr Ile Thr Phe Tyr Gly Asn Asp Val Gly Ala Thr Ser
 225 230 235 240

Tyr Ala Ala Lys Asp Val Asp Glu Arg Glu Lys His Pro Ala Lys Tyr
 245 250 255

30 Thr Val Asp Phe Asp Asn Lys Thr Met Asn Gly Lys Leu Ile Lys Asn
 260 265 270

Gln Tyr Val Arg Asn Lys Lys Asp Glu Pro Lys Lys Pro Leu Thr Ile
 275 280 285

35 Tyr Asp Ile Thr Ala Lys Leu Asp Gly Asn Arg Phe Thr Gly Ser Ala
 290 295 300

Lys Val Asn Pro Asp Leu Ala Lys Asn Leu Ala Gly Asn Glu Arg Leu
 305 310 315 320

Phe Phe His Ala Asp Ala Asp Gln Arg Leu Glu Gly Gly Phe Phe Gly
 325 330 335

40 Asp Asn Gly Glu Glu Leu Ala Gly Arg Phe Ile Ser Asn Asp Asn Ser
 340 345 350

32

Val Phe Gly Val Phe Ala Gly Lys Lys Thr Glu Thr Ala Asn Ala Ala
 355 360 365
 Asp Thr Lys Pro Ala Leu Pro Ser Gly Lys His Thr Lys Ile Leu Asp
 370 375 380
 5 Ser Leu Lys Ile Ser Val Asp Glu Ala Thr Asp Gly His Ala Arg Lys
 385 390 395 400
 Phe Ala Ile Ser Ser Met Pro Asp Phe Gly His Pro Asp Lys Leu Leu
 405 410 415
 10 Val Glu Gly Arg Glu Ile Pro Leu Val Asn Glu Glu Gln Ile Ile Lys
 420 425 430
 Leu Ala Asp Gly Arg Lys Met Thr Val Arg Ala Cys Cys Asp Phe Leu
 435 440 445
 Thr Tyr Val Lys Leu Gly Arg Ile Lys Thr Asp Arg Pro Ala Ser Lys
 450 455 460
 15 Pro Lys Ala Glu Asp Lys Gly Glu Asp Glu Glu Gly Ala Gly Val Asp
 465 470 475 480
 Asn Asp Glu Glu Ser Glu Asp Glu Ala Val Glu Asp Glu Gly Gly Glu
 485 490 495
 20 Glu Asp Glu Thr Ser Glu Glu Asp Asn Gly Glu Asp Glu Glu Ala Thr
 500 505 510
 Ala Glu Glu Glu Thr Glu Glu Val Asp Glu Ala Glu Glu Glu Val
 515 520 525
 Glu Glu Pro Glu Glu Lys Ser Pro Ala Glu Gly Asn Gly Gly Ser Gly
 530 535 540
 25 Ser Ile Leu Pro Ala Leu Glu Ala Ser Lys Gly Arg Asp Ile Asp Leu
 545 550 555 560
 Phe Leu Lys Gly Ile Arg Thr Ala Glu Thr Asp Ile Pro Gln Ser Gly
 565 570 575
 30 Thr Ala His Tyr Thr Gly Thr Trp Glu Ala Arg Ile Gly Lys Pro Ile
 580 585 590
 Gln Trp Asp Asn Gln Ala Asp Glu Lys Ala Ala Lys Ala Glu Phe Thr
 595 600 605
 Val Asp Phe Asp Lys Lys Ser Ile Ser Gly Lys Leu Thr Glu Gln Asn
 610 615 620
 35 Gly Val Glu Pro Ala Phe His Ile Glu Asp Gly Lys Ile Asp Gly Asn
 625 630 635 640
 Gly Phe His Ala Thr Ala Arg Thr Arg Glu Ser Gly Ile Asn Leu Ser
 645 650 655
 40 Gly Asn Gly Ser Thr Asp Pro Lys Thr Phe Gln Ala Ser Asn Leu Arg
 660 665 670
 Val Glu Gly Gly Phe Tyr Gly Pro Gln Ala Ala Glu Leu Gly Gly Thr
 675 680 685

33

Ile Phe Asn Asn Asp Gly Lys Ser Leu Ser Ile Thr Glu Asn Ile Glu
 690 695 700
 Asn Glu Ala Glu Ala Glu Val Glu Val Glu Ala Glu Ala Glu Val Glu
 705 710 715 720
 5 Val Glu Ala Asp Val Gly Lys Gln Leu Glu Pro Asp Glu Val Lys His
 725 730 735
 Lys Phe Gly Val Val Phe Gly Ala Lys Lys Asp Met Gln Glu Val Glu
 740 745 750
 Lys

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(2) INFORMATION FOR SEQ ID NO:9:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2124 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(B) STRAIN: Neisseria meningitidis strain 881607

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(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...2121

(D) OTHER INFORMATION:

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATG TGT AAA CCG AAT TAT GGC GGC ATT GTC TTG TTG CCC TTA CTT TTG 48
 Met Cys Lys Pro Asn Tyr Gly Gly Ile Val Leu Leu Pro Leu Leu Leu
 35 1 5 10 15
 GCA TCT TGC ATC GGC GGC AAT TTC GGC GTG CAG CCT GTT GTC GAA TCA 96
 Ala Ser Cys Ile Gly Gly Asn Phe Gly Val Gln Pro Val Val Glu Ser
 20 25 30
 40 ACG CCG ACC GCG TAC CCC GTC ACT TTC AAG TCT AAG GAC GTT CCC ACT 144
 Thr Pro Thr Ala Tyr Pro Val Thr Phe Lys Ser Lys Asp Val Pro Thr
 35 40 45

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|----|---|-----|
| | TCG CCT CCT GCC GGG TCT TCG GTA GAA ACC ACG CCG GTC AAC CGA CCC | 192 |
| | Ser Pro Pro Ala Gly Ser Ser Val Glu Thr Thr Pro Val Asn Arg Pro | |
| | 50 55 60 | |
| 5 | GCC GTT GGT GCG GCA ATG CGG CTG TTG AGA CGG AAT ATT GCA ACT TCT | 240 |
| | Ala Val Gly Ala Ala Met Arg Leu Leu Arg Arg Asn Ile Ala Thr Ser | |
| | 65 70 75 80 | |
| 10 | GAT AAG GAT GGC AAT GAT TTT CCA AAT AGC AAA CAA GCA GAA GAA AAG | 288 |
| | Asp Lys Asp Gly Asn Asp Phe Pro Asn Ser Lys Gln Ala Glu Glu Lys | |
| | 85 90 95 | |
| 15 | CTG TCG TTT AAA GAG GAA GAT ATC CTG TTT TTA TAC GGT TCC AAA AAA | 336 |
| | Leu Ser Phe Lys Glu Glu Asp Ile Leu Phe Leu Tyr Gly Ser Lys Lys | |
| | 100 105 110 | |
| 20 | GAT CAA CGT CAG CAG CTT AAA GAT AAA ATT CGT CAA CCA AAT CCT ACG | 384 |
| | Asp Gln Arg Gln Gln Leu Lys Asp Lys Ile Arg Gln Pro Asn Pro Thr | |
| | 115 120 125 | |
| 25 | GCA AGC ATT ACC ACA TCG GAA AAG AAA AAT AAA AAA TAT GAT TAT AAA | 432 |
| | Ala Ser Ile Thr Thr Ser Glu Lys Lys Asn Lys Lys Tyr Asp Tyr Lys | |
| | 130 135 140 | |
| 30 | TTT GTA GAT GCA GGT TAT GTA TAT ACT AAA GAC GGA AAA GAT GAA ATT | 480 |
| | Phe Val Asp Ala Gly Tyr Val Tyr Thr Lys Asp Gly Lys Asp Glu Ile | |
| | 145 150 155 160 | |
| 35 | GAG TGG ACT TCA AAT TAC AAG CAG TCT ACC AAC CCG TTT GGT TAT GAC | 528 |
| | Glu Trp Thr Ser Asn Tyr Lys Gln Ser Thr Asn Arg Phe Gly Tyr Asp | |
| | 165 170 175 | |
| 40 | GGT TTT GTA TAT TAT TCC GGA GAA CAT CCT TCG CAA TCT TTA CCG AGC | 576 |
| | Gly Phe Val Tyr Tyr Ser Gly Glu His Pro Ser Gln Ser Leu Pro Ser | |
| | 180 185 190 | |
| 45 | GCG GGA ACG GTG AAA TAT TCC GGC AAC TGG CAA TAT ATG ACC GAT GCC | 624 |
| | Ala Gly Thr Val Lys Tyr Ser Gly Asn Trp Gln Tyr Met Thr Asp Ala | |
| | 195 200 205 | |

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|----|---|------|
| | ATA CGT CAT CGA ACA GGA AAA GCA GGA GAT CCT AGC GAA GAT TTG GGT | 672 |
| | Ile Arg His Arg Thr Gly Lys Ala Gly Asp Pro Ser Glu Asp Leu Gly | |
| | 210 215 220 | |
| 5 | TAT ATC GTT TAT TAC GGT CAA AAT GTC GGA GCA ACT TCT TAT GCT GCG | 720 |
| | Tyr Ile Val Tyr Tyr Gly Gln Asn Val Gly Ala Thr Ser Tyr Ala Ala | |
| | 225 230 235 240 | |
| 10 | ACT GCC GAC GAC CGG GAG GGA AAA CAT CCT GCC GAA TAT ACG GTT AAT | 768 |
| | Thr Ala Asp Asp Arg Glu Gly Lys His Pro Ala Glu Tyr Thr Val Asn | |
| | 245 250 255 | |
| 15 | TTC GAC CAA AAA ACT CTG AAT GGC AAG CTG ATT AAA AAT CAG TAT GTG | 816 |
| | Phe Asp Gln Lys Thr Leu Asn Gly Lys Leu Ile Lys Asn Gln Tyr Val | |
| | 260 265 270 | |
| 20 | CAA AAG AGA GAT GAT CCT AAA AAA CCA CTG ACC ATT TAC GAC ATT ACT | 864 |
| | Gln Lys Arg Asp Asp Pro Lys Lys Pro Leu Thr Ile Tyr Asp Ile Thr | |
| | 275 280 285 | |
| 25 | GCA AAA TTG GAC GGC AAC CGC TTT ACC GGC AGT GCC AAA GTT AAC ACA | 912 |
| | Ala Lys Leu Asp Gly Asn Arg Phe Thr Gly Ser Ala Lys Val Asn Thr | |
| | 290 295 300 | |
| 30 | GAG GTG AAG ACG AAT CAC GCT GAT AAA GAA TAT TTG TTT TTC CAT ACC | 960 |
| | Glu Val Lys Thr Asn His Ala Asp Lys Glu Tyr Leu Phe Phe His Thr | |
| | 305 310 315 320 | |
| 35 | GAT GCC GAT CAG CGG CTT GAG GGC GGT TTT TTC GGC GAT AAG GGG GAA | 1008 |
| | Asp Ala Asp Gln Arg Leu Glu Gly Gly Phe Phe Gly Asp Lys Gly Glu | |
| | 325 330 335 | |
| 40 | GAG CTT GCC GGA CGG TTT ATC AGC AAC GAC AAC AGC GTA TTC GGC GTG | 1056 |
| | Glu Leu Ala Gly Arg Phe Ile Ser Asn Asp Asn Ser Val Phe Gly Val | |
| | 340 345 350 | |
| 45 | TTC GCA GGC AAA CAA AAA ACA GAG ACA GCA AAC GCA TCA GAT ACA AAT | 1104 |
| | Phe Ala Gly Lys Gln Lys Thr Glu Thr Ala Asn Ala Ser Asp Thr Asn | |
| | 355 360 365 | |
| 50 | CCT GCC CTG CCG TCT GGA AAA CAC ACC AAA ATC TTG GAT TCT CTA AAA | 1152 |
| | Pro Ala Leu Pro Ser Gly Lys His Thr Lys Ile Leu Asp Ser Leu Lys | |
| | 370 375 380 | |

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|----|---|------|
| 5 | ATT TCC GTT GAC GAG GCA AGT GGT GAA AAT CCC CGA CCG TTT GAG GTT | 1200 |
| | Ile Ser Val Asp Glu Ala Ser Gly Glu Asn Pro Arg Pro Phe Glu Val | |
| | 385 390 395 400 | |
| | TCC ACT ATG CCC GAT TTT GGT CAT CCC GAC AAA CTT CTT GTC GAA GGG | 1248 |
| | Ser Thr Met Pro Asp Phe Gly His Pro Asp Lys Leu Leu Val Glu Gly | |
| 10 | CGT GAA ATT CCT TTG GTA AAC AAA GAA CAA ACC ATC GAT CTT GCC GAC | 1296 |
| | Arg Glu Ile Pro Leu Val Asn Lys Glu Gln Thr Ile Asp Leu Ala Asp | |
| | 420 425 430 | |
| | GGC AGG AAA ATG ACC GTC CGT GCT TGT TGC GAC TTT TTG ACC TAT GTG | 1344 |
| | Gly Arg Lys Met Thr Val Arg Ala Cys Cys Asp Phe Leu Thr Tyr Val | |
| 15 | AAA CTC GGA CGG ATA AAA ACC GAA CGC CCC GCC GTC CAA CCG AAG GCG | 1392 |
| | Lys Leu Gly Arg Ile Lys Thr Glu Arg Pro Ala Val Gln Pro Lys Ala | |
| | 450 455 460 | |
| | CAG GAT GAA GAG GGG GAC GAA GAG GGT GTA GGC GTT GAT AAC GGT AAA | 1440 |
| | Gln Asp Glu Glu Gly Asp Glu Glu Gly Val Gly Val Asp Asn Gly Lys | |
| 20 | GAA AGC GAA GAC GAA ATC GGC GAT GAA GAA AGC ACC GGA GAC GAA GTC | 1488 |
| | Glu Ser Glu Asp Glu Ile Gly Asp Glu Glu Ser Thr Gly Asp Glu Val | |
| | 485 490 495 | |
| | GTA GAA GAT GAA GAC GAA GAT GAA GAC GAA GAA GAA ATC GAA GAA GAA | 1536 |
| | Val Glu Asp Glu Asp Glu Asp Glu Asp Glu Glu Glu Ile Glu Glu Glu | |
| 25 | CCT GAA GAA GAA GCT GAA GAG GAA GAA CCC GAA GAA GAA TTG CCG GCA | 1584 |
| | Pro Glu Glu Glu Ala Glu Glu Glu Glu Pro Glu Glu Glu Leu Pro Ala | |
| | 515 520 525 | |
| | GAA GAA GGC AAC GGC GGT TCA GGC AGC ATC CTG CCC ACT CCG GAA GCC | 1632 |
| | Glu Glu Gly Asn Gly Gly Ser Gly Ser Ile Leu Pro Thr Pro Glu Ala | |
| 30 | GAA GAA GGC AAC GGC GGT TCA GGC AGC ATC CTG CCC ACT CCG GAA GCC | 1632 |
| | Glu Glu Gly Asn Gly Gly Ser Gly Ser Ile Leu Pro Thr Pro Glu Ala | |
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(2) INFORMATION FOR SEQ ID NO:10:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 707 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(B) STRAIN: *Neisseria meningitidis* strain 881607

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

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Met Cys Lys Pro Asn Tyr Gly Gly Ile Val Leu Leu Pro Leu Leu Leu
 1             5             10             15
20 Ala Ser Cys Ile Gly Gly Asn Phe Gly Val Gln Pro Val Val Glu Ser
    20             25             30
Thr Pro Thr Ala Tyr Pro Val Thr Phe Lys Ser Lys Asp Val Pro Thr
    35             40             45
Ser Pro Pro Ala Gly Ser Ser Val Glu Thr Thr Pro Val Asn Arg Pro
25     50             55             60
Ala Val Gly Ala Ala Met Arg Leu Leu Arg Arg Asn Ile Ala Thr Ser
65             70             75             80
Asp Lys Asp Gly Asn Asp Phe Pro Asn Ser Lys Gln Ala Glu Glu Lys
    85             90             95
30 Leu Ser Phe Lys Glu Glu Asp Ile Leu Phe Leu Tyr Gly Ser Lys Lys
    100             105             110
Asp Gln Arg Gln Gln Leu Lys Asp Lys Ile Arg Gln Pro Asn Pro Thr
    115             120             125
Ala Ser Ile Thr Thr Ser Glu Lys Lys Asn Lys Lys Tyr Asp Tyr Lys
35     130             135             140
Phe Val Asp Ala Gly Tyr Val Tyr Thr Lys Asp Gly Lys Asp Glu Ile
145             150             155             160
Glu Trp Thr Ser Asn Tyr Lys Gln Ser Thr Asn Arg Phe Gly Tyr Asp
    165             170             175
40 Gly Phe Val Tyr Tyr Ser Gly Glu His Pro Ser Gln Ser Leu Pro Ser
    180             185             190
Ala Gly Thr Val Lys Tyr Ser Gly Asn Trp Gln Tyr Met Thr Asp Ala
    195             200             205

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39

Ile Arg His Arg Thr Gly Lys Ala Gly Asp Pro Ser Glu Asp Leu Gly
 210 215 220
 Tyr Ile Val Tyr Tyr Gly Gln Asn Val Gly Ala Thr Ser Tyr Ala Ala
 225 230 235 240
 5 Thr Ala Asp Asp Arg Glu Gly Lys His Pro Ala Glu Tyr Thr Val Asn
 245 250 255
 Phe Asp Gln Lys Thr Leu Asn Gly Lys Leu Ile Lys Asn Gln Tyr Val
 260 265 270
 10 Gln Lys Arg Asp Asp Pro Lys Lys Pro Leu Thr Ile Tyr Asp Ile Thr
 275 280 285
 Ala Lys Leu Asp Gly Asn Arg Phe Thr Gly Ser Ala Lys Val Asn Thr
 290 295 300
 Glu Val Lys Thr Asn His Ala Asp Lys Glu Tyr Leu Phe Phe His Thr
 305 310 315 320
 15 Asp Ala Asp Gln Arg Leu Glu Gly Gly Phe Phe Gly Asp Lys Gly Glu
 325 330 335
 Glu Leu Ala Gly Arg Phe Ile Ser Asn Asp Asn Ser Val Phe Gly Val
 340 345 350
 Phe Ala Gly Lys Gln Lys Thr Glu Thr Ala Asn Ala Ser Asp Thr Asn
 355 360 365
 20 Pro Ala Leu Pro Ser Gly Lys His Thr Lys Ile Leu Asp Ser Leu Lys
 370 375 380
 Ile Ser Val Asp Glu Ala Ser Gly Glu Asn Pro Arg Pro Phe Glu Val
 385 390 395 400
 25 Ser Thr Met Pro Asp Phe Gly His Pro Asp Lys Leu Leu Val Glu Gly
 405 410 415
 Arg Glu Ile Pro Leu Val Asn Lys Glu Gln Thr Ile Asp Leu Ala Asp
 420 425 430
 Gly Arg Lys Met Thr Val Arg Ala Cys Cys Asp Phe Leu Thr Tyr Val
 435 440 445
 30 Lys Leu Gly Arg Ile Lys Thr Glu Arg Pro Ala Val Gln Pro Lys Ala
 450 455 460
 Gln Asp Glu Glu Gly Asp Glu Glu Gly Val Gly Val Asp Asn Gly Lys
 465 470 475 480
 35 Glu Ser Glu Asp Glu Ile Gly Asp Glu Glu Ser Thr Gly Asp Glu Val
 485 490 495
 Val Glu Asp Glu Asp Glu Asp Glu Asp Glu Glu Glu Ile Glu Glu Glu
 500 505 510
 Pro Glu Glu Glu Ala Glu Glu Glu Glu Pro Glu Glu Glu Leu Pro Ala
 515 520 525
 40 Glu Glu Gly Asn Gly Gly Ser Gly Ser Ile Leu Pro Thr Pro Glu Ala
 530 535 540

Ser Lys Gly Arg Asp Ile Asp Leu Phe Leu Lys Gly Ile Arg Thr Ala
 545 550 555 560
 Glu Ala Asp Ile Pro Lys Asn Gly Thr Ala His Tyr Thr Gly Thr Trp
 565 570 575
 5 Glu Ala Arg Ile Gly Val Ser Asp Ser Gly Thr Ser Ile Gln Lys Asp
 580 585 590
 Ser Tyr Ala Asn Gln Gly Ala Lys Ala Glu Phe Thr Val Asp Phe Glu
 595 600 605
 Ala Lys Thr Val Ser Gly Met Leu Thr Glu Lys Asn Asp Thr Thr Pro
 10 610 615 620
 Ala Phe Tyr Ile Glu Lys Gly Val Ile Asp Gly Asn Gly Phe His Ala
 625 630 635 640
 Leu Ala His Thr Arg Glu Asn Gly Ile Asp Leu Ser Gly Gln Gly Ser
 645 650 655
 15 Thr Asn Pro Lys Asn Phe Lys Ala Asp Asn Leu Leu Val Thr Gly Gly
 660 665 670
 Phe Tyr Gly Pro Gln Ala Ala Glu Leu Gly Gly Asn Ile Ile Asp Ser
 675 680 685
 Asp Arg Lys Phe Gly Ala Val Phe Gly Ala Lys Lys Asp Asp Lys Glu
 20 690 695 700
 Ala Thr Arg
 705